RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/550,797
Source: IFW9
Date Processed by STIC: 8/28/06

ENTERED

IFWO

RAW SEQUENCE LISTING DATE: 08/28/2006
PATENT APPLICATION: **US/10/550,797** TIME: 09:26:32

Input Set : **F:\seq_210121_609uspc.app.txt**
Output Set: **N:\CRF4\08282006\J550797.raw**

<110> APPLICANT: Zehentner-Wilkinson, Barbara K.
Hayes, Dawn
Houghton, Raymond L.
<120> TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION AND MONITORING OF LUNG CANCER
<130> FILE REFERENCE: 210121.609USPC
<140> CURRENT APPLICATION NUMBER: US 10/550,797
C--> **<141> CURRENT FILING DATE: 2005-09-22**
<160> NUMBER OF SEQ ID NOS: 34
<170> SOFTWARE: Corixa Invention Disclosure Database
<210> SEQ ID NO: 1
<211> LENGTH: 3951
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
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55 gacttacacc ctgaacaata cccatcattc tctgcaagcc ctgaaagtga cagtgacctc 1860
56 tcgcgcctcc aactcagctg tgcccccagc cactgtggaa gcctttgtgg aaagagacag 1920
57 cctccatttt cctcatcctg tgatgattta tgccaatgtg aaacagggat tttatcccat 1980
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60 ttttttctcc tttgctgcaa atggtagata tagcttgaaa gtgcatgtca atcactctcc 2160
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63 ggagcgaaag tggggcttta gccgagtcag ctcaggaggc tccttttcag tgctgggagt 2340
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65 aaaagtagaa gaggaattga ccctatcttg gacagcacct ggagaagact ttgatcaggg 2460
66 ccaggctaca agctatgaaa taagaatgag taaaagtcta cagaatatcc aagatgactt 2520
67 taacaatgct attttagtaa atacatcaaa gcgaaatcct cagcaagctg gcatcaggga 2580
68 gatatttacg ttctcacccc aaatttccac gaatggacct gaacatcagc caaatggaga 2640
69 aacacatgaa agccacagaa tttatgttgc aatacgagca atggatagga actccttaca 2700
70 gtctgctgta tctaacattg cccaggcgcc tctgtttatt ccccccaatt ctgatcctgt 2760
71 acctgccaga gattatctta tattgaaagg agttttaaca gcaatgggtt tgataggaat 2820
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73 gaaagagaat ggaacaaaat tattataaat aaatatccaa agtgtcttcc ttcttagata 2940
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86 gttttaatac atatatgaac atatagtttt attcaattaa accaaagaag aggtcagcag 3720
87 ggagatacta acctttggaa atgattagct ggctctgttt tttggttaaa taagagtctt 3780
88 taatcctttc tccatcaaga gttacttacc aagggcaggg gaaggggat atagaggtcc 3840
89 caaggaaata aaaatcatct ttcatcttta attttactcc ttcctcttat ttttttaaaa 3900
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93 <211> LENGTH: 943
94 <212> TYPE: PRT
95 <213> ORGANISM: Homo sapiens
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100 Thr Leu Leu Val Ala Leu Ser Ser Glu Leu Pro Phe Leu Gly Ala Gly
101 20 25 30
102 Val Gln Leu Gln Asp Asn Gly Tyr Asn Gly Leu Leu Ile Ala Ile Asn
103 35 40 45

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106 Ile Thr Glu Ala Ser Phe Tyr Leu Phe Asn Ala Thr Lys Arg Arg Val
107 65                  70                  75                  80
108 Phe Phe Arg Asn Ile Lys Ile Leu Ile Pro Ala Thr Trp Lys Ala Asn
109                 85                  90                  95
110 Asn Asn Ser Lys Ile Lys Gln Glu Ser Tyr Glu Lys Ala Asn Val Ile
111             100                 105                 110
112 Val Thr Asp Trp Tyr Gly Ala His Gly Asp Asp Pro Tyr Thr Leu Gln
113         115                 120                 125
114 Tyr Arg Gly Cys Gly Lys Glu Gly Lys Tyr Ile His Phe Thr Pro Asn
115     130                 135                 140
116 Phe Leu Leu Asn Asp Asn Leu Thr Ala Gly Tyr Gly Ser Arg Gly Arg
117 145                 150                 155                 160
118 Val Phe Val His Glu Trp Ala His Leu Arg Trp Gly Val Phe Asp Glu
119                 165                 170                 175
120 Tyr Asn Asn Asp Lys Pro Phe Tyr Ile Asn Gly Gln Asn Gln Ile Lys
121             180                 185                 190
122 Val Thr Arg Cys Ser Ser Asp Ile Thr Gly Ile Phe Val Cys Glu Lys
123         195                 200                 205
124 Gly Pro Cys Pro Gln Glu Asn Cys Ile Ile Ser Lys Leu Phe Lys Glu
125     210                 215                 220
126 Gly Cys Thr Phe Ile Tyr Asn Ser Thr Gln Asn Ala Thr Ala Ser Ile
127 225                 230                 235                 240
128 Met Phe Met Gln Ser Leu Ser Ser Val Val Glu Phe Cys Asn Ala Ser
129                 245                 250                 255
130 Thr His Asn Gln Glu Ala Pro Asn Leu Gln Asn Gln Met Cys Ser Leu
131             260                 265                 270
132 Arg Ser Ala Trp Asp Val Ile Thr Asp Ser Ala Asp Phe His His Ser
133         275                 280                 285
134 Phe Pro Met Asn Gly Thr Glu Leu Pro Pro Pro Pro Thr Phe Ser Leu
135     290                 295                 300
136 Val Glu Ala Gly Asp Lys Val Val Cys Leu Val Leu Asp Val Ser Ser
137 305                 310                 315                 320
138 Lys Met Ala Glu Ala Asp Arg Leu Leu Gln Leu Gln Gln Ala Ala Glu
139                 325                 330                 335
140 Phe Tyr Leu Met Gln Ile Val Glu Ile His Thr Phe Val Gly Ile Ala
141             340                 345                 350
142 Ser Phe Asp Ser Lys Gly Glu Ile Arg Ala Gln Leu His Gln Ile Asn
143         355                 360                 365
144 Ser Asn Asp Asp Arg Lys Leu Leu Val Ser Tyr Leu Pro Thr Thr Val
145     370                 375                 380
146 Ser Ala Lys Thr Asp Ile Ser Ile Cys Ser Gly Leu Lys Lys Gly Phe
147 385                 390                 395                 400
148 Glu Val Val Glu Lys Leu Asn Gly Lys Ala Tyr Gly Ser Val Met Ile
149                 405                 410                 415
150 Leu Val Thr Ser Gly Asp Asp Lys Leu Leu Gly Asn Cys Leu Pro Thr
151             420                 425                 430
152 Val Leu Ser Ser Gly Ser Thr Ile His Ser Ile Ala Leu Gly Ser Ser
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Input Set : F:\seq_210121_609uspc.app.txt
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153         435                 440                 445
154 Ala Ala Pro Asn Leu Glu Glu Leu Ser Arg Leu Thr Gly Gly Leu Lys
155     450                 455                 460
156 Phe Phe Val Pro Asp Ile Ser Asn Ser Asn Ser Met Ile Asp Ala Phe
157 465                 470                 475                 480
158 Ser Arg Ile Ser Ser Gly Thr Gly Asp Ile Phe Gln Gln His Ile Gln
159                 485                 490                 495
160 Leu Glu Ser Thr Gly Glu Asn Val Lys Pro His His Gln Leu Lys Asn
161             500                 505                 510
162 Thr Val Thr Val Asp Asn Thr Val Gly Asn Asp Thr Met Phe Leu Val
163         515                 520                 525
164 Thr Trp Gln Ala Ser Gly Pro Pro Glu Ile Ile Leu Phe Asp Pro Asp
165     530                 535                 540
166 Gly Arg Lys Tyr Tyr Thr Asn Asn Phe Ile Thr Asn Leu Thr Phe Arg
167 545                 550                 555                 560
168 Thr Ala Ser Leu Trp Ile Pro Gly Thr Ala Lys Pro Gly His Trp Thr
169                 565                 570                 575
170 Tyr Thr Leu Asn Asn Thr His His Ser Leu Gln Ala Leu Lys Val Thr
171             580                 585                 590
172 Val Thr Ser Arg Ala Ser Asn Ser Ala Val Pro Pro Ala Thr Val Glu
173         595                 600                 605
174 Ala Phe Val Glu Arg Asp Ser Leu His Phe Pro His Pro Val Met Ile
175     610                 615                 620
176 Tyr Ala Asn Val Lys Gln Gly Phe Tyr Pro Ile Leu Asn Ala Thr Val
177 625                 630                 635                 640
178 Thr Ala Thr Val Glu Pro Glu Thr Gly Asp Pro Val Thr Leu Arg Leu
179                 645                 650                 655
180 Leu Asp Asp Gly Ala Gly Ala Asp Val Ile Lys Asn Asp Gly Ile Tyr
181             660                 665                 670
182 Ser Arg Tyr Phe Phe Ser Phe Ala Ala Asn Gly Arg Tyr Ser Leu Lys
183         675                 680                 685
184 Val His Val Asn His Ser Pro Ser Ile Ser Thr Pro Ala His Ser Ile
185     690                 695                 700
186 Pro Gly Ser His Ala Met Tyr Val Pro Gly Tyr Thr Ala Asn Gly Asn
187 705                 710                 715                 720
188 Ile Gln Met Asn Ala Pro Arg Lys Ser Val Gly Arg Asn Glu Glu Glu
189                 725                 730                 735
190 Arg Lys Trp Gly Phe Ser Arg Val Ser Ser Gly Gly Ser Phe Ser Val
191             740                 745                 750
192 Leu Gly Val Pro Ala Gly Pro His Pro Asp Val Phe Pro Pro Cys Lys
193         755                 760                 765
194 Ile Ile Asp Leu Glu Ala Val Lys Val Glu Glu Glu Leu Thr Leu Ser
195     770                 775                 780
196 Trp Thr Ala Pro Gly Glu Asp Phe Asp Gln Gly Gln Ala Thr Ser Tyr
197 785                 790                 795                 800
198 Glu Ile Arg Met Ser Lys Ser Leu Gln Asn Ile Gln Asp Asp Phe Asn
199                 805                 810                 815
200 Asn Ala Ile Leu Val Asn Thr Ser Lys Arg Asn Pro Gln Gln Ala Gly
201             820                 825                 830
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```
202 Ile Arg Glu Ile Phe Thr Phe Ser Pro Gln Ile Ser Thr Asn Gly Pro
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204 Glu His Gln Pro Asn Gly Glu Thr His Glu Ser His Arg Ile Tyr Val
205     850                 855                 860
206 Ala Ile Arg Ala Met Asp Arg Asn Ser Leu Gln Ser Ala Val Ser Asn
207 865                 870                 875                 880
208 Ile Ala Gln Ala Pro Leu Phe Ile Pro Pro Asn Ser Asp Pro Val Pro
209                 885                 890                 895
210 Ala Arg Asp Tyr Leu Ile Leu Lys Gly Val Leu Thr Ala Met Gly Leu
211             900                 905                 910
212 Ile Gly Ile Ile Cys Leu Ile Ile Val Val Thr His His Thr Leu Ser
213         915                 920                 925
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218 <211> LENGTH: 785
219 <212> TYPE: DNA
220 <213> ORGANISM: Homo sapiens
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225 tgtttctttg ccacggccgc agccgcggcg gccgcagccg ccgcagcggc agcgcagagc 180
226 gcgcagcagc agcagcagca gcagcagcag caggcgccgc agctgagacc ggcggccgac 240
227 ggccagccct caggggcgg tcacaagtca gcgcccaagc aagtcaagcg acagcgctcg 300
228 tcttcgcccg aactgatgcg ctgcaaacgc cggctcaact tcagcggctt tggctacagc 360
229 ctgccgcagc agcagccggc cgccgtggcg cgccgcaacg agcgcgagcg caaccgcgtc 420
230 aagttggtca acctgggctt tgccaccctt cgggagcacg tccccaacgg cgcggccaac 480
231 aagaagatga gtaaggtgga gacactgcgc tcggcggtcg agtacatccg cgcgctgcag 540
232 cagctgctgg acgagcatga cgcggtgagc gccgccttcc aggcaggcgt cctgtcgccc 600
233 accatctccc ccaactactc caacgacttg aactccatgg ccggctcgcc ggtctcatcc 660
234 tactcgtcgg acgagggctc ttacgacccg ctcagccccg aggagcagga gcttctcgac 720
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236 agcag                                                           785
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239 <211> LENGTH: 236
240 <212> TYPE: PRT
241 <213> ORGANISM: Homo sapiens
243 <400> SEQUENCE: 4
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247             20                  25                  30
248 Ala Thr Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Gln
249         35                  40                  45
250 Ser Ala Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ala Pro
251     50                  55                  60
252 Gln Leu Arg Pro Ala Ala Asp Gly Gln Pro Ser Gly Gly Gly His Lys
253 65                  70                  75                  80
254 Ser Ala Pro Lys Gln Val Lys Arg Gln Arg Ser Ser Ser Pro Glu Leu
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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date